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OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/006,869

DATE: 12/17/2001

TIME: 11:00:32

Input Set : A:\407c7.app.txt

Output Set: N:\CRF3\12172001\J006869.raw

P.S.

3 <110> APPLICANT: Blaschuk, Orest W:
 4 Symonds, James Matthew
 5 Gour, Barbara J.
 7 <120> TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
 8 CADHERIN-MEDIATED FUNCTIONS
 10 <130> FILE REFERENCE: 100086.407C7
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/006,869
 13 <141> CURRENT FILING DATE: 2001-12-03
 15 <160> NUMBER OF SEQ ID NOS: 4052
 17 <170> SOFTWARE: PatentIn Ver. 2.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 5
 21 <212> TYPE: PRT
 22 <213> ORGANISM: Unknown
 24 <220> FEATURE:
 25 <221> NAME/KEY: VARIANT
 26 <222> LOCATION: (2)
 27 <223> OTHER INFORMATION: Where Xaa is any amino acid
 29 <220> FEATURE:
 30 <223> OTHER INFORMATION: Description of Unknown Organism: Calcium Binding
 31 Motif in Extracellular domains of Classical
 32 Cadherins
 34 <400> SEQUENCE: 1
 W--> 35 Asp Xaa Asn Asp Asn
 36 1 5
 39 <210> SEQ ID NO: 2
 40 <211> LENGTH: 4
 41 <212> TYPE: PRT
 42 <213> ORGANISM: Unknown
 44 <220> FEATURE:
 45 <223> OTHER INFORMATION: Description of Unknown Organism: Calcium Binding
 46 Motif in Extracellular domains of Classical
 47 Cadherins
 49 <400> SEQUENCE: 2
 50 Leu Asp Arg Glu
 51 1
 54 <210> SEQ ID NO: 3
 55 <211> LENGTH: 9
 56 <212> TYPE: PRT
 57 <213> ORGANISM: Unknown
 59 <220> FEATURE:
 60 <221> NAME/KEY: VARIANT
 61 <222> LOCATION: (1)
 62 <223> OTHER INFORMATION: Residue is an independently selected amino acid
 64 <220> FEATURE:
 65 <221> NAME/KEY: VARIANT
 66 <222> LOCATION: (3)

ENTERED

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67 <223> OTHER INFORMATION: Residue is an independently selected amino acid
 69 <220> FEATURE:
 70 <221> NAME/KEY: VARIANT
 71 <222> LOCATION: (4)
 72 <223> OTHER INFORMATION: Where Xaa is Isoleucine, Leucine or Valine
 74 <220> FEATURE:
 75 <221> NAME/KEY: VARIANT
 76 <222> LOCATION: (5)
 77 <223> OTHER INFORMATION: Where Xaa is Aspartic Acid, Asparagine or Glutamic
 78 Acid
 80 <220> FEATURE:
 81 <221> NAME/KEY: VARIANT
 82 <222> LOCATION: (6)
 83 <223> OTHER INFORMATION: Residue is an independently selected amino acid
 85 <220> FEATURE:
 86 <221> NAME/KEY: VARIANT
 87 <222> LOCATION: (7)
 88 <223> OTHER INFORMATION: Residue is an independently selected amino acid
 90 <220> FEATURE:
 91 <221> NAME/KEY: VARIANT
 92 <222> LOCATION: (8)
 93 <223> OTHER INFORMATION: Where Xaa is Serine, Threonine or Asparagine
 95 <220> FEATURE:
 96 <223> OTHER INFORMATION: Description of Unknown Organism: Cell Adhesion
 97 Recognition Sequence of Nonclassical Cadherins
 99 <400> SEQUENCE: 3 /
 100 Xaa Phe Xaa Xaa Xaa Xaa Xaa Xaa Gly
 101 1 5
 104 <210> SEQ ID NO: 4
 105 <211> LENGTH: 110
 106 <212> TYPE: PRT
 107 <213> ORGANISM: Homo sapiens
 109 <400> SEQUENCE: 4
 110 Arg Ser Lys Arg Gly Trp Val Trp Asn Gln Phe Phe Val Ile Glu Glu
 111 1 5 10 15
 113 Tyr Thr Gly Pro Asp Pro Val Leu Val Gly Arg Leu His Ser Asp Ile
 114 20 25 30
 116 Asp Ser Gly Asp Gly Asn Ile Lys Tyr Ile Leu Ser Gly Glu Gly Ala
 117 35 40 45
 119 Gly Thr Ile Phe Val Ile Asp Asp Lys Ser Gly Asn Ile His Ala Thr
 120 50 55 60
 122 Lys Thr Leu Asp Arg Glu Glu Arg Ala Gln Tyr Thr Leu Met Ala Gln
 123 65 70 75 80
 125 Ala Val Asp Arg Asp Thr Asn Arg Pro Leu Glu Pro Pro Ser Glu Phe
 126 85 90 95
 128 Ile Val Lys Val Gln Asp Ile Asn Asp Asn Pro Pro Glu Phe
 129 100 105 110
 132 <210> SEQ ID NO: 5
 133 <211> LENGTH: 109

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134 <212> TYPE: PRT
135 <213> ORGANISM: Homo sapiens
137 <400> SEQUENCE: 5
138 Leu His Glu Thr Tyr His Ala Asn Val Pro Glu Arg Ser Asn Val Gly
139   1           5           10           15
141 Thr Ser Val Ile Gln Val Thr Ala Ser Asp Ala Asp Asp Pro Thr Tyr
142           20           25           30
144 Gly Asn Ser Ala Lys Leu Val Tyr Ser Ile Leu Glu Gly Gln Pro Tyr
145           35           40           45
147 Phe Ser Val Glu Ala Gln Thr Gly Ile Ile Arg Thr Ala Leu Pro Asn
148           50           55           60
150 Met Asp Arg Glu Ala Lys Glu Glu Tyr His Val Val Ile Gln Ala Lys
151  65           70           75           80
153 Asp Met Gly Gly His Met Gly Gly Leu Ser Gly Thr Thr Lys Val Thr
154           85           90           95
156 Ile Thr Leu Thr Asp Val Asn Asp Asn Pro Pro Lys Phe
157           100          105
160 <210> SEQ ID NO: 6
161 <211> LENGTH: 108
162 <212> TYPE: PRT
163 <213> ORGANISM: Homo sapiens
165 <400> SEQUENCE: 6
166 Arg Gln Lys Arg Asp Trp Ile Trp Asn Gln Met His Ile Asp Glu Glu
167   1           5           10           15
169 Lys Asn Thr Ser Leu Pro His His Val Gly Lys Ile Lys Ser Ser Val
170           20           25           30
172 Ser Arg Lys Asn Ala Lys Tyr Leu Leu Lys Gly Glu Tyr Val Gly Lys
173           35           40           45
175 Val Phe Arg Val Asp Ala Glu Thr Gly Asp Val Phe Ala Ile Glu Arg
176           50           55           60
178 Leu Asp Arg Glu Asn Ile Ser Glu Tyr His Leu Thr Ala Val Ile Val
179  65           70           75           80
181 Asp Lys Asp Thr Gly Glu Asn Leu Glu Thr Pro Ser Ser Phe Thr Ile
182           85           90           95
184 Lys Val His Asp Val Asn Asp Asn Trp Pro Val Phe
185           100          105
188 <210> SEQ ID NO: 7
189 <211> LENGTH: 110
190 <212> TYPE: PRT
191 <213> ORGANISM: Homo sapiens
193 <400> SEQUENCE: 7
194 Arg Ser Lys Arg Ser Trp Met Trp Asn Gln Phe Phe Leu Leu Glu Glu
195   1           5           10           15
197 Tyr Thr Gly Ser Asp Tyr Gln Tyr Val Gly Lys Leu His Ser Asp Gln
198           20           25           30
200 Asp Arg Gly Asp Gly Ser Leu Lys Tyr Ile Leu Ser Gly Asp Gly Ala
201           35           40           45
203 Gly Asp Leu Phe Ile Ile Asn Glu Asn Thr Gly Asp Ile Gln Ala Thr
204           50           55           60

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```

206 Lys Arg Leu Asp Arg Glu Glu Lys Pro Val Tyr Ile Leu Arg Ala Gln
207 65          70          75          80
209 Ala Ile Asn Arg Arg Thr Gly Arg Pro Val Glu Pro Glu Ser Glu Phe
210          85          90          95
212 Ile Ile Lys Ile His Asp Ile Asn Asp Asn Glu Pro Ile Phe
213          100          105          110
216 <210> SEQ ID NO: 8
217 <211> LENGTH: 109
218 <212> TYPE: PRT
219 <213> ORGANISM: Homo sapiens
221 <400> SEQUENCE: 8
222 Thr Lys Glu Val Tyr Thr Ala Thr Val Pro Glu Met Ser Asp Val Gly
223 1          5          10          15
225 Thr Phe Val Val Gln Val Thr Ala Thr Asp Ala Asp Asp Pro Thr Tyr
226          20          25          30
228 Gly Asn Ser Ala Lys Val Val Tyr Ser Ile Leu Gln Gly Gln Pro Tyr
229          35          40          45
231 Phe Ser Val Glu Ser Glu Thr Gly Ile Ile Lys Thr Ala Leu Leu Asn
232          50          55          60
234 Met Asp Arg Glu Asn Arg Glu Gln Tyr Gln Val Val Ile Gln Ala Lys
235 65          70          75          80
237 Asp Met Gly Gly Gln Met Gly Gly Leu Ser Gly Thr Thr Thr Val Asn
238          85          90          95
240 Ile Thr Leu Thr Asp Val Asn Asp Asn Pro Pro Arg Phe
241          100          105
244 <210> SEQ ID NO: 9
245 <211> LENGTH: 105
246 <212> TYPE: PRT
247 <213> ORGANISM: Homo sapiens
249 <400> SEQUENCE: 9
250 Ser Lys Leu Ala Tyr Ile Leu Gln Ile Arg Glu Asp Ala Gln Ile Asn
251 1          5          10          15
253 Thr Thr Ile Gly Ser Val Thr Ala Gln Asp Pro Asp Ala Ala Arg Asn
254          20          25          30
256 Pro Val Lys Tyr Ser Val Asp Arg His Thr Asp Met Asp Arg Ile Phe
257          35          40          45
259 Asn Ile Asp Ser Gly Asn Gly Ser Ile Phe Thr Ser Lys Leu Leu Asp
260          50          55          60
262 Arg Glu Thr Leu Leu Trp His Asn Ile Thr Val Ile Ala Thr Glu Ile
263 65          70          75          80
265 Asn Asn Pro Lys Gln Ser Ser Arg Val Pro Leu Tyr Ile Lys Val Leu
266          85          90          95
268 Asp Val Asn Asp Asn Ala Pro Glu Phe
269          100          105
272 <210> SEQ ID NO: 10
273 <211> LENGTH: 110
274 <212> TYPE: PRT
275 <213> ORGANISM: Gallus gallus
277 <400> SEQUENCE: 10

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278 Arg Thr Lys Arg Ser Trp Val Trp Asn Gln Phe Phe Val Leu Glu Glu
279   1           5           10           15
281 Tyr Met Gly Ser Asp Pro Leu Tyr Val Gly Lys Leu His Ser Asp Val
282           20           25           30
284 Asp Lys Gly Asp Gly Ser Ile Lys Tyr Ile Leu Ser Gly Glu Gly Ala
285           35           40           45
287 Ser Ser Ile Phe Ile Ile Asp Glu Asn Thr Gly Asp Ile His Ala Thr
288           50           55           60
290 Lys Arg Leu Asp Arg Glu Glu Gln Ala Tyr Tyr Thr Leu Arg Ala Gln
291   65           70           75           80
293 Ala His Asp Arg Leu Thr Asn Lys Pro Val Glu Pro Glu Ser Glu Phe
294           85           90           95
296 Val Ile Lys Ile Gln Asp Ile Asn Asp Asn Glu Pro Lys Phe
297           100          105          110
300 <210> SEQ ID NO: 11
301 <211> LENGTH: 109
302 <212> TYPE: PRT
303 <213> ORGANISM: Gallus gallus
305 <400> SEQUENCE: 11
306 Leu Asp Gly Pro Tyr Thr Ala Gly Val Pro Glu Met Ser Pro Val Gly
307   1           5           10           15
309 Thr Ser Val Val Gln Val Thr Ala Thr Asp Ala Asp Asp Pro Thr Tyr
310           20           25           30
312 Gly Asn Ser Ala Arg Val Val Tyr Ser Ile Leu Gln Gly Gln Pro Tyr
313           35           40           45
315 Phe Ser Val Glu Pro Lys Thr Gly Ile Ile Lys Thr Ala Leu Pro Asn
316           50           55           60
318 Met Asp Arg Glu Ala Lys Asp Gln Tyr Leu Leu Val Ile Gln Ala Lys
319   65           70           75           80
321 Asp Met Val Gly Gln Asn Gly Gly Leu Ser Gly Thr Thr Ser Val Thr
322           85           90           95
324 Val Thr Leu Thr Asp Val Asn Asp Asn Pro Pro Arg Phe
325           100          105
328 <210> SEQ ID NO: 12
329 <211> LENGTH: 105
330 <212> TYPE: PRT
331 <213> ORGANISM: Gallus gallus
333 <400> SEQUENCE: 12
334 Thr Ser Arg Leu Tyr Ser Met Val Val Ser Glu Ala Ala Lys Val Gly
335   1           5           10           15
337 Thr Ile Ile Gly Thr Val Ala Ala His Asp Pro Asp Ala Ser Asn Ser
338           20           25           30
340 Pro Val Arg Tyr Ser Ile Asp Arg Asn Thr Asp Leu Glu Arg Tyr Phe
341           35           40           45
343 Asn Ile Asp Ala Asn Ser Gly Val Ile Thr Thr Ala Lys Ser Leu Asp
344           50           55           60
346 Arg Glu Thr Asn Ala Val His Asn Ile Thr Val Leu Ala Met Glu Ser
347   65           70           75           80
349 Gln Asn Pro Ala Gln Ile Gly Arg Gly Tyr Val Ala Ile Thr Ile Leu

```

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\407c7.app.txt

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L:12 M:270 C: Current Application Number differs, Wrong Format

L:35 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:1310 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46

L:1340 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47

L:1436 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53

L:1459 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54

L:1482 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55

L:1507 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56

L:1530 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57

L:1755 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71

L:1805 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72